



- 34 -

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: NeuTec Pharma plc
- (B) STREET: Clinical Sciences Building, Central  
Manchester Healthcare
- (C) CITY: Trust, Oxford Road, Manchester
- (E) COUNTRY: GB
- (F) POSTAL CODE (ZIP): M13 9WL

(ii) TITLE OF INVENTION: Treatment and Diagnosis of Infections of  
Gram

Positive Cocci

(iii) NUMBER OF SEQUENCES: 15

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9614274.0
- (B) FILING DATE: 06-JUL-1996

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid

- 35 -

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGTGGATT GGTATGGAC ATCCGTTTTG AACAGTAGAT TCACTTATCA GCCGAATACA  
60  
CCATTTGAAC AAAGAGCCTT ATTTGACATC AATAAGAAGA TCAAAGGAAA CAGTTATACT  
120  
GCATTAGTAG GGCATACCGG AAGCGGGAAA TCAACCTTAC TTCAGCATTG GAATGCGCTT  
180  
GTTAAGCCAA CAAGCGGTAC AGTCCATATT GGAGAACGAG ATATTCAGCC GGATACGGAT  
240  
AATAAGAATT TAAAGCCCAT CCGAAAAAAA GTTGGCATCG TCTTTCAGTT TCCAGAAGCA  
300  
CAGCTATTTCG AAGAAACGGT AGCAAAAGAC ATTGCTTTTCG GTCCTAAAAA CTTTGGTGTC  
360  
AGCGAAGAAG AAGCACTAGT CCTAGCAAAA GAAACATTAG AACAAGTTGG GCTGGATGAA  
420  
AGCTATTTGG AACGTTTCGCC ATTTGAACTT TCAGGAGGGC AAATGCGTAG AGTAGCAATC  
480  
GCTGGTGTGC TTGCCATGAG GCCGGAAGTA CTTGTATTGG ATGAACCAAC GGCAGGACTT  
540

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

- 36 -

Met Val Asp Trp Leu Trp Thr Ser Val Leu Asn Ser Arg Phe Thr Tyr  
 1 5 10 15

Gln Pro Asn Thr Pro Phe Glu Gln Arg Ala Leu Phe Asp Ile Asn Lys  
 20 25 30

Lys Ile Lys Gly Asn Ser Tyr Thr Ala Leu Val Gly His Thr Gly Ser  
 35 40 45

Gly Lys Ser Thr Leu Leu Gln His Leu Asn Ala Leu Val Lys Pro Thr  
 50 55 60

Ser Gly Thr Val His Ile Gly Glu Arg Asp Ile Gln Pro Asp Thr Asp  
 65 70 75 80

Asn Lys Asn Leu Lys Pro Ile Arg Lys Lys Val Gly Ile Val Phe Gln  
 85 90 95

Phe Pro Glu Ala Gln Leu Phe Glu Glu Thr Val Ala Lys Asp Ile Ala  
 100 105 110

Phe Gly Pro Lys Asn Phe Gly Val Ser Glu Glu Glu Ala Leu Val Leu  
 115 120 125

Ala Lys Glu Thr Leu Glu Gln Val Gly Leu Asp Glu Ser Tyr Leu Glu  
 130 135 140

Arg Ser Pro Phe Glu Leu Ser Gly Gly Gln Met Arg Arg Val Ala Ile  
 145 150 155 160

Ala Gly Val Leu Ala Met Arg Pro Glu Val Leu Val Leu Asp Glu Pro  
 165 170 175

Thr Ala Gly Leu

- 37 -

180

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Gly Xaa Gly Lys Ser Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Thr Gly Ser Gly Lys Ser Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid

- 39 -

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Arg Val Ala Ile Ala Gly Val Leu

1

5

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATTTAAAGAA ATTATTAATA AAAAAATTGA ATTAGGATGT ACAGCTATGG CCATTTTAA

60

ATATATAGAG AAAAAGGGTT ATGAAGGTAA ATATACTATT CTACGAGAAT ACTGTAAAAA

120

TAAAAAACAA AATGAGACTA AAAAAGCAAC TATACGCGTA GAACTAATC CCGGTATAGC

180

TGCTCAAGTA GACTGGAAAG AAGATATGGT AATGCATGAT AAGTTTGGCA GAACTTATCA

240

ATTCAACATC TTTCTTTACG TTCTACACTA TTCAAAAATG AAGTATATCA CATTAACTTG

300

- 40 -

GGATAGAAAA CAAGATACCT TATTGAATG TTTAAAAGAC GCTTTTGAAT ACACCGAAGG  
360

GGTTCCAAAA GAAATCTGGT TCGATAATAT GAGAACTGTA GTTGATCGAC CTAGAACACA  
420

ATATAAAAAA GTCGTCTTTA ATAATTTATT TTATCAATTT AGTAAGGATG CCAACTTTGA  
480

ACCTATTGCT TGTAGACCCT ATCGTCCTCA AACAAAAGGG TCTGTTGAAT CATTAGCTAA  
540

ATTTGTTGAA CAGCGTTTAA GACCATACGA TTATGAATTT TATGATGCTG TAGAACTTAT  
600

TGGGCTAGTA AACGATTTAT GTCACGAATT GAATCACTTA GAAATTTTAC AAGCAACAGA  
660

ACAACGACCT ATCGACGTTT TCAATTATGA AGAAAAAGAA CATTTAAATT CTTTTAATGC  
720

CAAGTTACTA GATACTTACA TCGAAAATGA GTGTATAAGA ATCGTTTCTA AAGAATCGAT  
780

GATTAACTTT AGAAAAGGTA AATACTCGGT ACCTACTAAA TACATTGGTG AAGAAGTACA  
840

AGTGATATTC AATAATTCTA CTGATGAATT GCTGATTTAT TATGATGGTG AATTAATAAG  
900

ACGGCATAAT CTATCCGAAA GAAAATTTAA TTATATCGTT GAAGATATGA GTGAAATATT  
960

AAAATCAGAT GTATTTAAAC ATAAGGATGA CAAAGAAATT CTTACGTATA TAGAAAATTC  
1020

ATTATTACTG TATGACGAAA TTTAGGAGGA CTTTCGATGA ATACGAACCA TCAAAAATTA  
1080

CTTAATAACT TTGAAATATT AAAACTAAAA AAATTCAAAG ATTATTATCC AAACATATTT  
1140

GAATTACTTT CTAAAAATGA GAAATCTTTA ACTGAAATAT TGATTGATTT AACGGAAAAA  
1200

GAAATAGAAT ATCAATCAGA ATTAAATTT AAACGTGCTG TGAATTCAGC ACGTTTCCCT  
1260

AAAATAAAAT ATTTACATGA TTTTGATTTT ATGTTTCAAC CTAAGTATAA ATCAACAAGA  
1320

- 41 -

AATACTCACT TTAAATCTA TGCATTTTTT AGAAGATAGT ATAAATATTT GTTTCTAGTA  
 1380  
 ATAGTGGTGT TGGTAAACA CACCTAGCAA TCTCATTAGG AATAGAGGCA TGTTAGCAAA  
 1440  
 ATATAAAGAC TAGATCC  
 1457

(2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Lys Glu Ile Ile Asn Lys Lys Ile Glu Leu Gly Cys Thr Ala Met  
 1 5 10 15

Ala Ile Phe Lys Tyr Ile Glu Lys Lys Gly Tyr Glu Gly Lys Tyr Thr  
 20 25 30

Ile Leu Arg Glu Tyr Cys Lys Asn Lys Lys Gln Asn Glu Thr Lys Lys  
 35 40 45

Ala Thr Ile Arg Val Glu Thr Asn Pro Gly Ile Ala Ala Gln Val Asp  
 50 55 60

Trp Lys Glu Asp Met Val Met His Asp Lys Phe Gly Arg Thr Tyr Gln  
 65 70 75 80

Phe Asn Ile Phe Leu Tyr Val Leu His Tyr Ser Lys Met Lys Tyr Ile

95

100 105 110

.. 115 120 125

130	135	140
-----	-----	-----

145                      150                      155                      160

165 170 175

180 185 190

195	200	205
-----	-----	-----

210                      215                      220

225                      230                      235                      240

245                      250                      255



- 43 -

```

260
265
270
Lys Tyr Ile Gly Glu Glu Val Gln Val Ile Phe Asn Asn Ser Thr Asp
275
280
285
Glu Leu Leu Ile Tyr Tyr Asp Gly Glu Leu Ile Arg Arg His Asn Leu
290
295
300
Ser Glu Arg Lys Phe Asn Tyr Ile Val Glu Asp Met Ser Glu Ile Leu
305
310
315
320
Lys Ser Asp Val Phe Lys His Lys Asp Asp Lys Glu Ile Leu Thr Tyr
325
330
335
Ile Glu Asn Ser Leu Leu Leu Tyr Asp Glu Ile
340
345

```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met	Asn	Thr	Asn	His	Gln	Lys	Leu	Leu	Asn	Asn	Phe	Glu	Ile	Leu	Lys
1				5					10						15
Leu	Lys	Lys	Phe	Lys	Asp	Tyr	Tyr	Pro	Asn	Tyr	Ile	Glu	Leu	Leu	Ser
				20					25					30	
Lys	Asn	Glu	Lys	Ser	Leu	Thr	Glu	Ile	Leu	Ile	Asp	Leu	Thr	Glu	Lys

- 44 -

35 40 45

Glu Ile Glu Tyr Gln Ser Glu Leu Lys Phe Lys Arg Ala Val Asn Ser  
50 55 60

Ala Arg Phe Pro Lys Ile Lys Tyr Leu His Asp Phe Asp Phe Met Phe  
65 70 75 80

Gln Pro Lys Tyr Lys Ser Thr Arg Asn Thr His Phe Lys Ile Tyr Ala  
85 90 95

Phe Phe Arg Arg  
100

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Gln Val Asp Trp Lys Glu  
1 5

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

- 45 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Phe Glu Tyr Thr Glu Gly Val Pro Lys

1

5

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Thr Lys Ser Gly Val Glu

1

5

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ser Gly Val Gly Lys Thr His Leu Ala

1

5